

GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds
(without alignments)
564,351 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706
Sequence: 1 MGIGRSGGRGALGVLLA.....KFMKKMKHCEPTQSVFK 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/pcodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/pcodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/pcodata/1/1aa/7 COMB.pep.*
4: /cgn2_6/pcodata/1/1aa/PCUS_COMB.pep.*
5: /cgn2_6/pcodata/1/1aa/RE_COMB.pep.*
6: /cgn2_6/pcodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1701	99.7	314	2	US-08-937-067-7
2	1691.5	99.2	313	2	US-09-514-885-1
3	1691.5	99.2	313	2	US-09-949-016-6239
4	1657.5	97.2	313	2	US-09-546-043-3
5	1657.5	97.2	313	2	US-09-546-043-4
6	1629	95.5	314	2	US-09-087-031E-3
7	1614.5	94.6	313	2	US-09-087-031E-4
8	1267.5	74.3	267	2	US-09-546-043-6
9	1171	68.6	246	2	US-09-546-043-8
10	971	56.9	229	2	US-09-546-043-8
11	924.5	54.2	317	2	US-08-937-067-6
12	924.5	54.2	317	2	US-09-949-016-6300
13	911.5	53.4	305	2	US-09-949-016-7706
14	887.5	52.0	195	2	US-09-546-043-5
15	605.5	35.5	295	2	US-08-937-067-2
16	598	35.1	295	2	US-09-999-833A-415
17	598	35.1	295	2	US-10-020-445A-415
18	597	35.0	295	2	US-09-148-545-179
19	597	35.0	295	2	US-09-621-011-179
20	597	35.0	296	2	US-09-148-545-237
21	597	35.0	296	2	US-09-621-011-237
22	594	34.8	109	2	US-09-087-031E-19
23	508.5	29.8	295	2	US-08-893-654B-6
24	436	25.6	212	2	US-08-937-067-4
25	409.5	24.0	280	2	US-08-893-654B-4
26	387	22.7	281	2	US-08-893-654B-2
27	353	20.7	113	2	US-09-087-031E-24

28	272.5	16.0	572	2	US-08-937-067-13	Sequence 13, Appl
29	262.5	15.4	537	2	US-08-937-067-11	Sequence 11, Appl
30	262	15.4	319	2	US-10-014-055-7	Sequence 7, Appl
31	258	15.1	318	2	US-10-014-055-8	Sequence 8, Appl
32	258	15.1	319	2	US-10-028-051A-7	Sequence 7, Appl
33	258	15.1	565	2	US-08-937-067-8	Sequence 8, Appl
34	253.5	14.9	325	2	US-10-014-055-2	Sequence 2, Appl
35	253.5	14.9	325	2	US-10-028-051A-2	Sequence 2, Appl
36	252	14.8	318	2	US-08-878-474-3	Sequence 3, Appl
37	248	14.5	319	2	US-10-028-051A-8	Sequence 8, Appl
38	247.5	14.5	323	2	US-08-878-474-7	Sequence 7, Appl
39	247.5	14.5	325	2	US-08-878-474-9	Sequence 9, Appl
40	247.5	14.5	325	2	US-09-976-594-479	Sequence 479, App
41	247.5	14.5	325	2	US-10-014-055-4	Sequence 4, Appl
42	247.5	14.5	325	2	US-10-028-051A-4	Sequence 4, Appl
43	247.5	14.5	371	2	US-09-949-016-7544	Sequence 7544, Ap
44	244	14.3	111	2	US-10-014-055-5	Sequence 5, Appl
45	244	14.3	111	2	US-10-028-051A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-937-067-7
; Sequence 7, Application US/08937067
; Patent No. 643355
; GENERAL INFORMATION:
; APPLICANT: Umehany, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-937-067-7
Query Match 99.7%; Score 1701; DB 2; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-174;
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGIGRSGGRGALGVLLAALGAAALAVGASRYDVSPQSDIGPQSGRFTTKPQCVD 60
DB 1 MGIGRSGGRGALGVLLAALGAAALAVGASRYDVSPQSDIGPQSGRFTTKPQCVD 60

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QY 61 IPADRLCHNVGKVKVLPNLLHEHTMAVKKOASWVPLLNKNCAGTQVFLCSLPAFV 120
DB 61 IPADRLCHNVGKVKVLPNLLHEHTMAVKKOASWVPLLNKNCAGTQVFLCSLPAFV 120
QY 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIANTPPNATEASRP 180
DB 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIANTPPNATEASRP 180
QY 181 QGTVCPDNLKSEALIEHLCASEFALRMKIKKVKENGDKKLVKPKKKPLKGLPIKX 240
DB 181 QGTVCPDNLKSEALIEHLCASEFALRMKIKKVKENGDKKLVKPKKKPLKGLPIKX 240
QY 241 KDLKGLVYLKNGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMKX 300
DB 241 KDLKGLVYLKNGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMKX 300
QY 301 MKNHECPTFGSVFK 314
DB 301 MKNHECPTFGSVFK 314

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RESULT 2

```

US-09-514-885-1
; Sequence 1, Application US/09514885
; Patent No. 6656461
; GENERAL INFORMATION:
; APPLICANT: D'Armentio, Jeanline
; APPLICANT: Imai, Kazuaki
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 58483, add
; CURRENT APPLICATION NUMBER: US/09/514, 885
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-514-885-1

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Query Match 99.2%; Score 1691.5; DB 2; Length 313;
Best Local Similarity 99.7%; Pred. No. 3.6e-173;
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGIGRSGRRGALGVLLALGALLAVGSASEYDVVSFQSDIGFYQSGRFTTKPQCVD 60
DB 1 MGIGRSGRRG-ALGVLLALGALLAVGSASEYDVVSFQSDIGFYQSGRFTTKPQCVD 59
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DB 61 IPADRLCHNVGKVKVLPNLLHEHTMAVKKOASWVPLLNKNCAGTQVFLCSLPAFV 119
QY 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIANTPPNATEASRP 180
DB 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIANTPPNATEASRP 179
QY 181 QGTVCPDNLKSEALIEHLCASEFALRMKIKKVKENGDKKLVKPKKKPLKGLPIKX 240
DB 181 QGTVCPDNLKSEALIEHLCASEFALRMKIKKVKENGDKKLVKPKKKPLKGLPIKX 239
QY 241 KDLKGLVYLKNGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMKX 300
DB 240 KDLKGLVYLKNGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMKX 299
QY 301 MKNHECPTFGSVFK 314
DB 300 MKNHECPTFGSVFK 313

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RESULT 3
US-09-949-016-6299
; Sequence 6299, Application US/09949016

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```

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6299
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6299

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Query Match 99.2%; Score 1691.5; DB 2; Length 313;
Best Local Similarity 99.7%; Pred. No. 3.6e-173;
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGIGRSGRRGALGVLLALGALLAVGSASEYDVVSFQSDIGFYQSGRFTTKPQCVD 60
DB 1 MGIGRSGRRG-ALGVLLALGALLAVGSASEYDVVSFQSDIGFYQSGRFTTKPQCVD 59
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DB 61 IPADRLCHNVGKVKVLPNLLHEHTMAVKKOASWVPLLNKNCAGTQVFLCSLPAFV 119
QY 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIANTPPNATEASRP 180
DB 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIANTPPNATEASRP 179
QY 181 QGTVCPDNLKSEALIEHLCASEFALRMKIKKVKENGDKKLVKPKKKPLKGLPIKX 240
DB 181 QGTVCPDNLKSEALIEHLCASEFALRMKIKKVKENGDKKLVKPKKKPLKGLPIKX 239
QY 241 KDLKGLVYLKNGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMKX 300
DB 240 KDLKGLVYLKNGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMKX 299
QY 301 MKNHECPTFGSVFK 314
DB 300 MKNHECPTFGSVFK 313

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RESULT 4
US-09-546-043-3
; Sequence 3, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey et al.
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-3

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Query Match 97.2%; Score 1657.5; DB 2; Length 313;
Best Local Similarity 97.5%; Pred. No. 1.6e-169;
Matches 306; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

```

XX New secreted frizzled-related protein-1-binding peptide, for enhancing or
PT stimulating osteoclast differentiation or to modify T-cell activity in a
PT subject with e.g. abnormal bone remodeling, achondroplasia or
PT osteopetrosis.
XX
XX Example, Page 74-75; 81pp; English.
XX
XX The invention relates to a purified peptide that binds to secreted
CC frizzled-related protein (sFRP)-1. The peptide is useful for enhancing or
CC stimulating osteoclast differentiation, or to modify T-cell activity in a
CC subject with abnormal bone remodeling, achondroplasia, Albright's
CC osteodystrophy or osteopetrosis. The sFRP-1 is useful for inhibiting
CC osteoclast formation in a subject with a bone disorder or unwanted bone
CC resorption, e.g. postmenopausal osteoporosis, Paget's disease, lytic bone
CC metastases, multiple myeloma, rheumatoid arthritis or hypercalcemia of
CC malignancy. Modulating T-cell activity is useful in subjects suspected of
CC having toxic shock, sepsis, graft-versus-host reactions or acute
CC inflammatory reactions. The immunostimulatory sFRP-1-binding peptide is
CC useful in activating the immune system against bacterial, viral and
CC parasitic infections, and in the treatment of human immunodeficiency
CC virus (HIV). The present sequence represents a human sFRP-1 netrin
CC homology domain
CC
XX Sequence 141 AA;
SQ
XX
XX Query Match 100.0%; Score 78; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KKEGDKKIVPKKK 15
DB 52 KKEGDKKIVPKKK 66
XX
XX RESULT 2
XX ID AAY48493 standard; protein; 148 AA.
XX AAY48493;
XX
XX 08-DEC-1999 (first entry)
XX
XX Human breast tumour-associated protein 38.
XX
XX Expressed sequence tag; EST; human; breast; cancer; cyrostatic;
XX medicaments; gene therapy; treatment; fat metabolism.
XX
XX Homo sapiens.
XX
XX DE19813835-A1.
XX
XX 23-SEP-1999.
XX
XX 20-MAR-1998; 98DE-01013835.
XX
XX 20-MAR-1998; 98DE-01013835.
XX
XX (META-) METRAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX WPI; 1999-528979/45.
XX
XX N-PSDB; AA233577.
XX
XX Human nucleic acid sequences and protein products from normal breast
PT tissue, useful for breast cancer therapy.
XX
XX Claim 26; 175; 206pp; German.
XX
XX This invention describes novel human nucleic acid sequences from normal
CC breast tissue which have cyrostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can

CC be used to express proteins, which can be used as tools to find an
CC activity against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer and for treating illnesses associated with
CC fat metabolism. AAY48456-748539 represent protein fragments encoded by
CC the expressed sequence tags described in the method of the invention
XX
XX Sequence 148 AA;
SQ
XX
XX Query Match 100.0%; Score 78; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KKEGDKKIVPKKK 15
DB 51 KKEGDKKIVPKKK 65
XX
XX RESULT 3
XX ID ADR09139 standard; protein; 178 AA.
XX ADR09139;
XX
XX 04-NOV-2004 (first entry)
XX
XX
XX Human protein useful for treating neurological disease Seq 2645.
XX
XX human; oligo-capping method; diagnostic marker; gene therapy;
XX osteoporosis; neurological disease; Alzheimer's disease;
XX Parkinson's disease; dementia; short memory; cancer;
XX sense or motor function; emotional reaction; fear response; panic;
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cyrostatic;
XX tranquilliser.
XX
XX Homo sapiens.
XX
XX EP1447413-A2.
XX
XX 18-AUG-2004.
XX
XX 12-FEB-2004; 2004EP-00003145.
XX
XX 14-FEB-2003; 2003JP-00102207.
XX
XX 09-MAY-2003; 2003JP-0011452.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
XX Wakamatsu A, Ishii S, Nagai K, Irie R;
XX WPI; 2004-583265/57.
XX
XX N-PSDB; ADR07183.
XX
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 2645; 2686pp; English.
XX
XX This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNA. The present invention
CC describes an immunosay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,

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OW protein - protein search, using sw model

Run on: May 5, 2006, 13:50:51 ; Search time 229 Seconds
(without alignments)
967.406 Million cell updates/sec

Title: US-10-666-851-2
Perfect score: 1706
Sequence: 1 MGIGRSGRGGRAALGVLLA.....KNFMKMKMKNCPTFQSVFK 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query	Length	DB	ID	Description
1	1706	100.0	314	1	SPRP1_HUMAN	O6N474 homo sapien
2	1626	95.3	314	2	O505A2_MOUSE	O505A2 mus musculu
3	1623	95.1	314	1	SPRP1_MOUSE	O6C4U3 mus musculu
4	1607	94.2	308	1	SPRP1_BOVIN	O19116 bos taurus
5	1489	87.3	314	1	SPRP1_CHICK	O9D6Q4 gallus galli
6	1100.5	64.5	306	2	O6GZK1_ORYLA	O6GZK1 oryzias lat
7	1092.5	64.0	321	2	O4SKX3_TESTNG	O4SKX3 tetraodon n
8	1084	63.5	311	2	O9Y124_XENLA	O9Y124 xenopus lae
9	1070.5	62.7	310	2	O6YNR8_BRARE	O6YNR8 brachydantio
10	1012	59.3	296	2	O7T2K9_BRARE	O7T2K9 brachydantio
11	955.5	56.0	311	2	O4RGR2_TESTNG	O4RGR2 tetraodon n
12	947.5	55.5	281	2	O568X0_BRARE	O568X0 brachydantio
13	946	55.5	315	2	O6GL50_XENLA	O6GL50 xenopus tro
14	945	55.4	315	2	O640J3_XENLA	O640J3 xenopus lae
15	942.5	55.2	315	2	O6AWG4_XENLA	O6AWG4 xenopus lae
16	924.5	54.2	317	1	SPRP5_HUMAN	O6T447 homo sapien
17	922.5	54.1	314	1	SPRP5_MOUSE	O6WU66 mus musculu
18	916.5	53.7	315	1	SPRP5_BOVIN	O6X6C1 bos taurus
19	844	49.5	158	1	SPRP1_RAT	O9P168 rattus norv
20	718	42.1	178	2	O6ZSL4_HUMAN	O6ZSL4 homo sapien
21	658.5	38.6	295	2	O6P8B8_XENLA	O6P8B8 xenopus tro
22	649	38.0	295	2	O4SS00_TESTNG	O4SS00 tetraodon n
23	645.5	37.8	298	2	O7ZXM6_XENLA	O7ZXM6 xenopus lae
24	629	36.9	282	2	O6JHC7_BRARE	O6JHC7 brachydantio
25	610	35.8	294	1	SPRP2_CANFA	O6J3H1 canis famil
26	610	35.8	365	2	O4H2U5_CIOIN	O4H2U5 ctiona inres
27	605.5	35.5	292	1	SPRP2_CHICK	O6I8A6 gallus galli
28	605.5	35.5	295	1	SPRP2_MOUSE	P9Z299 mus musculu
29	602	35.3	295	1	SPRP2_HUMAN	O9G6H1 homo sapien
30	595.5	34.9	283	2	O9B6G6_RABIT	O9B6G6 corycolagus
31	541.5	31.7	307	2	O42397_CHICK	O42397 gallus galli

32	515	30.2	300	2	O6P2E8_XENLA	O6P2E8 xenopus tro
33	508.5	29.8	295	2	O9I897_XENLA	O9I897 xenopus lae
34	463	27.1	293	2	O4H2U4_CIOIN	O4H2U4 ctiona inres
35	433	25.4	115	2	O90ZG8_BRARE	O90ZG8 brachydantio
36	413	24.2	281	2	O73821_XENLA	O73821 xenopus lae
37	412	24.2	130	2	O5ZK37_CHICK	O5ZK37 gallus galli
38	409.5	24.0	280	2	O9IAU5_XENLA	O9IAU5 xenopus lae
39	395	23.2	282	2	O4RS17_TESTNG	O4RS17 tetraodon n
40	392.5	23.0	284	2	O90ZA6_AMBER	O90ZA6 ambystoma m
41	390.5	22.9	261	2	O6IUE1_CAER	O6IUE1 caenorhabdi
42	385	22.6	260	2	O9GUP5_CAERL	O9GUP5 caenorhabdi
43	369.5	21.7	282	2	O7SX78_BRARE	O7SX78 brachydantio
44	369.5	21.7	289	2	O504J9_BRARE	O504J9 brachydantio
45	295	17.3	592	1	FZD1_CHICK	O57328 gallus galli

ALIGNMENTS

RESULT 1
SPRP1_HUMAN STANDARD, PRT; 314 AA.
ID SPRP1_HUMAN
AC O6N474; 000546; O14779;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Secreted Frlizled-related protein 1 precursor (SPRP-1) (Frlizled-related protein 1) (FRP-1) (Secreted apoptosis-related protein 2) (SARP-2).
GN Name=SPRP1; Synonyms=FRP, FRP1, SARP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Embryonic lung fibroblast;
RC MEDLINE=97338093; PubMed=9192640; DOI=10.1073/pnas.94.13.6770;
RA Finch P.W., He X., Kelley M.J., Uren A., Schaudies R.P., Poyescu N.C., Rudnikoff S., Aaronson S.A., Varmus H.E., Rubin J.S.;
RT "Purification and molecular cloning of a secreted, Frlizled-related antagonist of Wnt action.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:6770-6775(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=Heart;
RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M., Fitzpatrick P.A., Klefer M.C., Tomei L.D., Umansky S.R.;
RT "SARpe: a family of secreted apoptosis-related proteins.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA], AND INDUCTION.
RX PubMed=9724099;
RA Zhou Z., Wang J., Han X., Zhou J., Linder S.;
RT "Up-regulation of human secreted Frlizled homolog in apoptosis and its down-regulation in breast tumors.";
RT Int. J. Cancer 78:95-99(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Stausberg R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maniseta K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.B.,
RA Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Pringle C.,
RA Baka S.S., Iqbalilano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Roark S.A., McKernan K.J., Meleik J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulik S.W.,

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:54:06 ; Search time 39 seconds
(without alignments)
774.668 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706

Sequence: 1 MGIRSEGGRRGALGVLLA.....KNFMKKMKHCEPTFQSVF 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	917.5	53.8	317	JB0175	freezled protein-1
2	602	35.3	295	JB0174	freezled protein-2
3	276.5	16.2	574	JB0339	freezled-7 protein
4	273.5	16.0	568	JB0339	freezled-1 protein
5	271.5	15.9	537	JB0339	freezled protein 4
6	265	15.5	647	JB0337	freezled-1 protein
7	264	15.5	581	JB0340	gene freezled prot
8	258	15.1	565	JB0338	freezled-2 protein
9	256.5	15.0	581	JB0338	freezled-2 protein
10	252.5	14.8	641	JB0338	freezled-2 protein
11	237.5	13.9	550	JB0335	freezled-2 protein
12	228.5	13.4	694	JB0335	freezled-2 protein
13	223.5	13.1	197	JB0335	freezled-2 protein
14	215	12.6	666	JB0335	freezled-2 protein
15	215	12.6	706	JB0335	freezled-2 protein
16	201	11.8	605	JB0335	freezled-2 protein
17	201	11.8	1113	JB0335	freezled-2 protein
18	170.5	10.0	1774	JB0335	freezled-2 protein
19	133.5	7.8	526	JB0335	freezled-2 protein
20	132.5	7.8	579	JB0335	freezled-2 protein
21	125	7.3	793	JB0335	freezled-2 protein
22	107.5	6.3	549	JB0335	freezled-2 protein
23	97	5.7	785	JB0335	freezled-2 protein
24	97	5.7	2228	JB0335	freezled-2 protein
25	96.5	5.7	1024	JB0335	freezled-2 protein
26	96.5	5.7	1150	JB0335	freezled-2 protein
27	93.5	5.5	1474	JB0335	freezled-2 protein
28	93	5.5	527	JB0335	freezled-2 protein
29	92.5	5.4	1051	JB0335	freezled-2 protein

30	91	5.3	260	2	T01837	hypothetical prote
31	91	5.3	527	2	A42032	epidermal growth f
32	91	5.3	1008	2	C84679	hypothetical prote
33	91	5.3	1077	2	T21800	hypothetical prote
34	91	5.3	1223	1	TVC1V	epidermal growth f
35	90.5	5.3	1751	2	T09394	gag-pro-pol polypr
36	89.5	5.2	792	2	A70476	ATP-dependent DNA
37	88	5.2	718	2	T51488	hypothetical prote
38	88	5.2	1051	2	S55259	TIF1 protein - mou
39	87.5	5.1	1097	2	A56138	transcription fact
40	87.5	5.1	4152	2	T31102	filamentous hemagg
41	87.5	5.1	4919	2	T31105	hypothetical prote
42	87	5.1	578	2	C64452	restriction modifi
43	87	5.1	1699	2	T14074	complement compone
44	86.5	5.1	623	2	A49112	sodium-glucose cot
45	86.5	5.1	1001	2	S30385	G9a protein - huma

ALIGNMENTS

RESULT 1
JB0175
freezled protein-1b - human
C/Species: Homo sapiens (man)
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C/Accession: JB0175
R/Hu, B./Zhu, Y.: Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res Commun. 247, 287-293, 1998
A/Title: Tissue restricted expression of two human fibro in preadipocytes and pancreas.
A/Reference number: JB0174; PMID:98308108; PMID:9642118
A/Molecule type: mRNA
A/Residues: 1-317 <HUA>
A/Cross-references: UNIPROT:O14780; UNIPARC:UP10000158811
C/Genetics:
A/Map: hPRP-1b
A/Map position: 5q14.3-q12.1

Query Match 53.8%; Score 917.5; DB 2; Length 317;

Best Local Similarity 56.3%; Pred. No. 56-69; Matches 178; Conservative 51; Mismatches 78; Indels 9; Gaps 6;

QY	1	MGIRSEGGRRGALGVLLAALAVGSASBYDVVSFGSDIGPYGSRFTYKPPQCV	60
DB	1	MRBAAAAGVTRTAAALL--LGALHMAPACBETHYGMQAB--PLH-GRSYSGPPQCLD	55
QY	61	IPADLRICNANVGYKQVLPMLBHEBTMAEYKQASVPLANKCNAGTGVFLCSLPAPV	120
DB	56	IPADLRICNANVGYKQVLPMLBHEBTMAEYKQASVPLANKCNAGTGVFLCSLPAPV	115
QY	121	CLDRPIYPCRMGLCAVAVDSCEPVMOFPFGYPMPLKCDKRP-BGDVCIANTPPNATKASK	179
DB	116	CLDRPIYPCRMGLCAVAVDSCEPVMOFPFGYPMPLKCDKRP-BGDVCIANTPPNATKASK	174
QY	180	PGSTTVCPDNEILKBAITLHLCASBPALRMKIKYKKNKGDKTV--PKKKPLKGP	237
DB	175	PVPTKICACQEMHSDADGLMEQCSSDFVYKMKIKIKINGRKILGAKKKKLKPGP	234
QY	238	IKKKDLKLVLYLKNAGDCCHOLDNLSHFLPMGRKYSQYLLTAHKKDKKKKKK	297
DB	235	LKKRDKRLVLYLKNAGDCCHOLDNLSHFLPMGRKYSQYLLTAHKKDKKKKKK	294
QY	298	MKGKMKHCEPTFQSVF 313	
DB	295	VKEMSTPCSLTYPPF 310	

RESULT 2
JB0174
freezled protein-2 - human
C/Species: Homo sapiens (man)
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

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OM protein - protein search, using SW model

Run on: May 5, 2006, 13:59:36 ; Search time 27 Seconds
(without alignments)
538.274 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706
Sequence: 1 MGGRSGGRGALGVLLA.....KNFMKMKHCEPTQSVFK 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep1:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep1:*
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8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep1:*
9: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1691.5	99.2	413	US-10-821-234-989	Sequence 989, App
2	605.5	35.5	295	US-11-067-121-2	Sequence 2, App1
3	602	35.3	295	US-11-067-121-1	Sequence 11, App1
4	602	35.3	295	US-11-051-720-1701	Sequence 1701, App
5	598	35.1	295	US-10-216-161A-415	Sequence 415, App
6	389.5	22.8	180	US-11-051-720-1306	Sequence 1306, App
7	298	17.5	117	US-11-054-281-306	Sequence 306, App
8	290	17.0	566	US-11-054-281-93	Sequence 93, App1
9	280	16.4	530	US-11-054-281-94	Sequence 94, App1
10	271.5	15.9	537	US-10-511-937-2607	Sequence 2607, App
11	271.5	15.9	537	US-11-152-366-43	Sequence 43, App1
12	271.5	15.9	537	US-11-169-041-132	Sequence 132, App
13	271.5	15.9	537	US-11-169-041-134	Sequence 134, App
14	268.5	15.7	580	US-11-054-281-95	Sequence 95, App1
15	267.5	15.7	592	US-11-054-281-127	Sequence 127, App
16	266.5	15.6	595	US-11-054-281-92	Sequence 92, App1
17	262	15.4	591	US-11-054-281-36	Sequence 36, App1
18	261.5	15.3	591	US-11-054-281-128	Sequence 128, App
19	259.5	15.2	188	US-11-152-366-249	Sequence 249, App
20	258	15.1	352	US-11-054-281-126	Sequence 126, App1
21			319	US-11-184-005-7	Sequence 7, App1

22	256.5	15.0	581	US-11-067-231-153	Sequence 153, App
23	256.5	15.0	581	US-11-054-281-22	Sequence 22, App1
24	256.5	15.0	581	US-11-054-281-91	Sequence 91, App1
25	253.5	14.9	325	US-11-184-005-2	Sequence 2, App1
26	251	14.7	577	US-11-054-281-130	Sequence 130, App
27	248	14.5	319	US-11-184-005-8	Sequence 8, App1
28	247.5	14.5	325	US-11-184-005-4	Sequence 4, App1
29	244	14.3	111	US-11-184-005-5	Sequence 5, App1
30	243	14.2	111	US-11-184-005-6	Sequence 6, App1
31	243	14.2	549	US-11-054-281-129	Sequence 129, App
32	237	13.9	346	US-11-054-281-97	Sequence 97, App1
33	236	13.8	348	US-11-054-281-69	Sequence 69, App1
34	236	13.8	348	US-11-054-281-98	Sequence 98, App1
35	235.5	13.8	351	US-11-054-281-100	Sequence 100, App
36	234.5	13.7	585	US-11-127-877-63	Sequence 63, App1
37	234	13.7	348	US-11-054-281-99	Sequence 99, App1
38	233	13.7	346	US-11-301-554-329	Sequence 329, App
39	233	13.7	346	US-11-186-284-189	Sequence 189, App1
40	233	13.7	346	US-11-054-281-24	Sequence 24, App1
41	233	13.7	346	US-11-054-281-96	Sequence 96, App1
42	201	11.8	113	US-11-067-811-4	Sequence 4, App1
43	194	11.4	1042	US-11-067-811-1	Sequence 1, App1
44	137.5	8.1	116	US-11-152-366-283	Sequence 283, App
45	137.5	8.1	433	US-11-152-366-44	Sequence 44, App1

ALIGNMENTS

RESULT 1
US-10-821-234-989
; Sequence 989, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 989
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-989

Query Match	99.2%	Score 1691.5;	DB 9;	Length 413;
Best Local Similarity	99.7%	Pred. No. 1e-152;		
Matches 313;	Conservative	0;	Mismatches 0;	Indels 1; Gaps 1;
QY	1	MGGRSGGRGALGVLLAAGNALAVGSASRDYVSPQSDIGPYQSGRFYTKPPQCV	60	
DB	101	MGGRSGGRGALGVLLAAGNALAVGSASRDYVSPQSDIGPYQSGRFYTKPPQCV	159	
QY	61	IPADLRLCHNVGKRVNPLLEHETMAVYKQDASSMVLNKNKCHAGTQVPLCSLFAVY	120	
DB	160	IPADLRLCHNVGKRVNPLLEHETMAVYKQDASSMVLNKNKCHAGTQVPLCSLFAVY	219	
QY	121	CLDRPYTPGKWLCEAVRDSCEPVMQFPGFYTPMLKCDKFPBGDVCIAATPPVATASXP	180	
DB	220	CLDRPYTPGKWLCEAVRDSCEPVMQFPGFYTPMLKCDKFPBGDVCIAATPPVATASXP	279	
QY	181	OGTTVPCCDNELKSAITIEHLCASEFALRMKIKVYKKNQDKKIVPKKKKPKLGLPIKX	240	
DB	280	OGTTVPCCDNELKSAITIEHLCASEFALRMKIKVYKKNQDKKIVPKKKKPKLGLPIKX	339	
QY	241	KDKKLVLLKNGADPCHQDLNLSHHPLIMGRKVSQYLLTAIHRMKKKNKBFKNFMKK	300	

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OM protein - protein search, using SW model

Run on: May 5, 2006, 13:58:41 ; Search time 164 Seconds
(without alignments)
799.990 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706
Sequence: 1 MGIRSGRGGRRGALGVLLA.....KNFMKKMKNNHCPTFGSVFK 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
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2	1706	100.0	314 4 US-10-666-851-2	Sequence 2, App1
3	1706	100.0	314 4 US-10-788-792-148	Sequence 148, App
4	1701	99.7	314 4 US-10-146-474-7	Sequence 7, App1
5	1701	99.7	314 4 US-10-301-764-7	Sequence 7, App1
6	1701	99.7	314 5 US-10-756-149-5611	Sequence 5611, App
7	1691.5	99.2	313 3 US-09-796-008-2	Sequence 2, App1
8	1691.5	99.2	313 4 US-10-138-434A-4	Sequence 4, App1
9	1691.5	99.2	313 4 US-10-666-851-7	Sequence 7, App1
10	1691.5	99.2	313 5 US-10-786-720-43	Sequence 43, App1
11	1691.5	99.2	313 5 US-10-817-525-2	Sequence 2, App1
12	1691.5	99.2	313 5 US-10-847-972-77	Sequence 77, App1
13	1657.5	97.2	313 4 US-10-425-586-3	Sequence 3, App1
14	1657.5	97.2	313 4 US-10-466-136-3	Sequence 3, App1
15	1657.5	97.2	338 4 US-10-425-586-4	Sequence 4, App1
16	1657.5	97.2	338 4 US-10-466-136-4	Sequence 4, App1
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18	1267.5	74.3	267 4 US-10-425-586-7	Sequence 7, App1
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20	1171	68.6	246 4 US-10-425-586-6	Sequence 6, App1
21	1171	68.6	246 4 US-10-466-136-6	Sequence 6, App1
22	971	56.9	229 4 US-10-425-586-8	Sequence 8, App1
23	971	56.9	229 4 US-10-466-136-8	Sequence 8, App1
24	924.5	54.2	317 4 US-10-146-474-6	Sequence 6, App1
25	924.5	54.2	317 4 US-10-338-604-2	Sequence 2, App1
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27	924.5	54.2	317 5 US-10-768-566-1	Sequence 1, App1

28	922.5	54.1	314 4 US-10-338-604-5	Sequence 5, App1
29	887.5	52.0	195 4 US-10-425-586-5	Sequence 5, App1
30	887.5	52.0	195 4 US-10-466-136-5	Sequence 5, App1
31	762	44.7	141 4 US-10-466-136-13	Sequence 13, App1
32	622	36.5	109 4 US-10-138-434A-19	Sequence 19, App1
33	605.5	35.5	295 3 US-09-934-483A-1	Sequence 1, App1
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35	605.5	35.5	295 4 US-10-146-474-2	Sequence 2, App1
36	605.5	35.5	295 4 US-10-301-764-2	Sequence 2, App1
37	605.5	35.5	295 5 US-10-847-972-81	Sequence 81, App1
38	605.5	35.5	295 5 US-10-432-256-5	Sequence 5, App1
39	602.5	35.3	377 4 US-10-106-698-6382	Sequence 6382, App
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41	602	35.3	295 4 US-10-177-293-142	Sequence 142, App
42	602	35.3	295 4 US-10-295-027-1345	Sequence 107, App
43	602	35.3	295 5 US-10-783-528-107	Sequence 78, App1
44	602	35.3	295 5 US-10-847-972-78	Sequence 2, App1
45	602	35.3	295 5 US-10-432-256-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-10-138-434A-3
Sequence 3, Application US/10138434A
Publication No. US20030175864A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: Rubin, Jeffrey S.
APPLICANT: Finch, Paul
APPLICANT: Aaronson, Stuart
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN FRP AND FRAGMENTS THEREOF
FILE REFERENCE: 4239-62520
CURRENT APPLICATION NUMBER: US/10138,434A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 09/087,031
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: US 60/050,495
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: US 60/050,417
PRIOR FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-138-434A-3
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Best Local Similarity 100.0%; Pred. No. 8.9e-159;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 CLRPPIYPCRWLCEAVYDSCRPVMOFGFTWPRMLKCDKPRSDVCIAMTPNATASRP 180
1 QGTTVCPCDNLKSEALILEHLCASRPALMKIKYKKGNDKKIYPKKKKPKLKLPIKK 240
1 QGTTVCPCDNLKSEALILEHLCASRPALMKIKYKKGNDKKIYPKKKKPKLKLPIKK 240
181 QGTTVCPCDNLKSEALILEHLCASRPALMKIKYKKGNDKKIYPKKKKPKLKLPIKK 240
181 QGTTVCPCDNLKSEALILEHLCASRPALMKIKYKKGNDKKIYPKKKKPKLKLPIKK 240
241 KDLKGLVLYLKNADPCRNQDLNLSHNFLLMKRKYVSQYLLTAIHKMKKKKPKFKMKK 300

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds
(without alignments)
564.351 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706

Sequence: 1 MGIRSGGRRGALGVLLA.....KNFMKKMKHCEPTQSVK 314

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1657.5	97.2	313	2	US-09-546-043-3
5	1657.5	97.2	313	2	US-09-546-043-4
6	1629	95.5	314	2	US-09-087-031B-3
7	1614.5	94.6	313	2	US-09-087-031B-4
8	1267.5	74.3	267	2	US-09-546-043-7
9	1171	68.6	246	2	US-09-546-043-6
10	971	56.9	229	2	US-08-546-043-8
11	924.5	54.2	317	2	US-08-937-067-6
12	924.5	54.2	317	2	US-09-949-016-6300
13	911.5	53.4	305	2	US-09-949-016-7706
14	887.5	52.0	195	2	US-09-546-043-5
15	605.5	35.5	295	2	US-08-937-067-2
16	598	35.1	295	2	US-09-999-833A-415
17	598	35.1	295	2	US-10-020-445A-415
18	597	35.0	295	2	US-09-148-545-179
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20	597	35.0	296	2	US-09-148-545-237
21	597	35.0	296	2	US-09-621-011-237
22	594	34.8	109	2	US-09-087-031B-19
23	508.5	29.8	295	2	US-08-893-654B-6
24	436	25.6	212	2	US-08-937-067-4
25	409.5	24.0	280	2	US-08-893-654B-4
26	387	22.7	281	2	US-08-893-654B-2
27	353	20.7	113	2	US-09-087-031B-24

28	272.5	16.0	572	2	US-08-937-067-13	Sequence 13, Appl
29	262.5	15.4	537	2	US-08-937-067-11	Sequence 11, Appl
30	262	15.4	319	2	US-10-014-055-7	Sequence 7, Appl
31	258	15.1	318	2	US-10-014-055-8	Sequence 8, Appl
32	258	15.1	319	2	US-10-028-051A-7	Sequence 7, Appl
33	258	15.1	319	2	US-08-937-067-8	Sequence 8, Appl
34	253.5	14.9	325	2	US-10-014-055-2	Sequence 2, Appl
35	253.5	14.9	325	2	US-10-028-051A-2	Sequence 2, Appl
36	252	14.8	319	2	US-08-878-474-3	Sequence 3, Appl
37	248	14.5	319	2	US-10-028-051A-8	Sequence 8, Appl
38	247.5	14.5	323	2	US-08-878-474-7	Sequence 7, Appl
39	247.5	14.5	325	2	US-08-878-474-9	Sequence 9, Appl
40	247.5	14.5	325	2	US-09-976-594-479	Sequence 479, App
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42	247.5	14.5	325	2	US-10-028-051A-4	Sequence 4, Appl
43	247.5	14.5	371	2	US-09-849-016-7544	Sequence 7544, Ap
44	244	14.3	111	2	US-10-014-055-5	Sequence 5, Appl
45	244	14.3	111	2	US-10-028-051A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-937-067-7
Sequence 7, Application US/08937067
Patent No. 6431155

GENERAL INFORMATION:

APPLICANT: Umansky, Samu1

TITLE OF INVENTION: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 314 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-937-067-7

Query Match 99.7%; Score 1701; DB 2; Length 314;

Best Local Similarity 99.7%; Pred. No. 3.5e-174;

Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MGIRSGGRRGALGVLLAAGALLAVGASAEVDYVSFSDIGPGVSGRFTYKPPCCVD 60

1 MGIRSGGRRGALGVLLAAGALLAVGASAEVDYVSFSDIGPGVSGRFTYKPPCCVD 60

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OM protein - protein search, using SW model

Run on: May 5, 2006, 14:09:22 ; Search time 29 Seconds
(without alignments)
42.763 Million cell updates/sec

Title: US-10-666-851-2_COPY_217_231
Perfect score: 78
Sequence: 1 KXENGDKXIVPKKK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	78	100.0	267	US-09-546-043-7	Sequence 7, App1
3	78	100.0	313	US-09-087-0318-4	Sequence 4, App1
4	78	100.0	313	US-09-546-043-3	Sequence 1, App1
5	78	100.0	313	US-09-514-885-1	Sequence 6299, App
6	78	100.0	313	US-09-949-016-6299	Sequence 7, App1
7	78	100.0	314	US-08-937-067-7	Sequence 3, App1
8	78	100.0	314	US-09-087-0318-3	Sequence 4, App1
9	78	100.0	338	US-09-546-043-4	Sequence 4, App1
10	53	67.9	108	US-09-319-588C-6	Sequence 706, App
11	46	59.0	1014	US-09-949-016-7706	Sequence 6, App1
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15	45	57.7	334	US-09-248-796A-16963	Sequence 34052, A
16	44	56.4	144	US-09-107-433-3451	Sequence 48269, A
17	43	55.1	316	US-09-270-767-49259	Sequence 6872, App
18	43	55.1	316	US-09-513-999C-6072	Sequence 3938, App
19	43	55.1	106	US-09-621-976-3938	Sequence 14797, A
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22	42	53.8	1588	PCT-US93-07261-15	Sequence 3859, App
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29	41	52.6	219	US-09-134-001C-5651	Sequence 5651, App
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31	41	52.6	515	US-09-488-039A-10635	Sequence 10635, A
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38	40	51.3	120	US-09-415-868-114	Sequence 114, App
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67	40	51.3	1003	US-10-290-579A-192	Sequence 192, App
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96	39	50.0	85	US-09-513-999C-5823	Sequence 5823, App
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OM protein - protein search, using sw model

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(Without alignments)
57.856 Million cell updates/sec

Title: US-10-666-851-2_COPY_217_231
Perfect score: 78
Sequence: 1 KKENGGKIVPKKKK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	413	9	US-10-821-234-989
2	43.5	55.8	502	11	US-11-087-099-8879
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4	42	53.8	500	9	US-10-517-151-4
5	42	53.8	540	11	US-11-087-099-690
6	42	53.8	540	11	US-11-087-099-4162
7	42	53.8	541	11	US-11-087-099-2152
8	41	52.6	268	11	US-11-079-463-8502
9	41	52.6	278	11	US-11-079-463-6742
10	41	52.6	375	11	US-11-096-568A-21506
11	41	52.6	409	9	US-10-533-811-57
12	41	52.6	472	11	US-11-045-004-999
13	41	52.6	474	11	US-11-096-568A-21505
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18	40	51.3	35	11	US-11-096-725-1
19	40	51.3	259	11	US-11-079-463-6740
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23	40	51.3	1003	11	US-11-204-755-7	Sequence 7, App1
24	40	51.3	1003	11	US-11-204-755-9	Sequence 9, App1
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29	39	50.0	152	11	US-11-172-740-144	Sequence 144, App
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31	39	50.0	177	11	US-11-096-568A-25724	Sequence 25724, A
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61	37	47.4	148	11	US-11-096-568A-975	Sequence 975, App
62	37	47.4	153	9	US-10-689-742-42	Sequence 42, App1
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64	37	47.4	169	11	US-11-096-568A-973	Sequence 973, App
65	37	47.4	179	9	US-10-793-626-1092	Sequence 1092, Ap
66	37	47.4	222	11	US-11-096-568A-7170	Sequence 7170, Ap
67	37	47.4	222	9	US-10-793-626-498	Sequence 498, App
68	37	47.4	252	9	US-10-793-626-1368	Sequence 1368, Ap
69	37	47.4	259	11	US-11-096-568A-7169	Sequence 7169, Ap
70	37	47.4	282	11	US-11-188-298-11537	Sequence 11537, A
71	37	47.4	295	11	US-11-096-568A-34149	Sequence 34149, A
72	37	47.4	314	11	US-11-096-568A-34148	Sequence 34148, A
73	37	47.4	335	11	US-11-096-568A-34147	Sequence 34147, A
74	37	47.4	351	11	US-11-096-568A-34146	Sequence 34146, A
75	37	47.4	355	11	US-11-096-568A-34145	Sequence 34145, A
76	37	47.4	392	11	US-11-096-568A-34144	Sequence 34144, A
77	37	47.4	408	11	US-11-188-298-17882	Sequence 17882, A
78	37	47.4	430	11	US-11-126-313-35	Sequence 35, App1
79	37	47.4	430	11	US-11-126-313-36	Sequence 36, App1
80	37	47.4	504	11	US-11-087-099-1053	Sequence 1053, App
81	37	47.4	554	11	US-11-098-686-11102	Sequence 11102, Ap
82	37	47.4	560	11	US-11-087-099-5820	Sequence 5820, Ap
83	37	47.4	851	8	US-10-511-937-2597	Sequence 2597, App
84	37	47.4	1026	11	US-11-169-041-205	Sequence 205, App
85	37	47.4	1078	11	US-11-096-568A-30451	Sequence 30451, A
86	37	47.4	1116	11	US-11-096-568A-30450	Sequence 30450, A
87	37	47.4	1133	11	US-11-096-568A-30449	Sequence 30449, A
88	37	47.4	1130	11	US-11-086-482-1	Sequence 1, App1
89	37	47.4	1130	11	US-11-192-341-23	Sequence 23, App1
90	37	47.4	2344	9	US-10-330-773-627	Sequence 627, App
91	37	47.4	2801	9	US-10-330-773-630	Sequence 630, App
92	36.5	46.8	954	11	US-11-079-463-10024	Sequence 10024, A
93	36	46.2	124	11	US-11-172-740-1758	Sequence 1758, Ap
94	36	46.2	155	11	US-11-072-512-3937	Sequence 3937, Ap

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OM protein - protein search, using sw model

Run on: May 5, 2006, 14:06:21 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-666-851-2_COPY_217_231
Perfect score: 78
Sequence: 1 KKGNGDKIVPKKK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 500 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	59.0	205	2 T20990	hypothetical prote
2	46	59.0	279	2 T20987	hypothetical prote
3	46	59.0	397	2 T20013	hypothetical prote
4	46	59.0	3488	2 T34418	hypothetical prote
5	45	57.7	65	2 C69792	hypothetical prote
6	45	57.7	317	2 J80175	freezied protein-1
7	44	56.4	502	2 T22045	hypothetical prote
8	43.5	55.8	502	2 T14286	embryogenic callus
9	43	55.1	132	2 T48278	hypothetical prote
10	43	55.1	175	2 T05669	hypothetical prote
11	43	55.1	245	2 T50339	hypothetical prote
12	43	55.1	690	2 E72337	translacton initia
13	43	55.1	1196	2 T33832	protein-tyrosine k
14	43	55.1	1278	2 A71609	probable secreted
15	42	53.8	95	2 G97706	hypothetical prote
16	42	53.8	183	2 A35270	ribosomal protein
17	42	53.8	288	2 S26495	transcription fact
18	42	53.8	295	2 B86371	hypothetical prote
19	42	53.8	367	2 T39172	cyclin-dependent k
20	42	53.8	625	2 A90127	hypothetical prote
21	42	53.8	734	2 T23647	DNA topoisomerase
22	42	53.8	751	2 S65469	hypothetical prote
23	42	53.8	806	2 T23648	hypothetical prote
24	42	53.8	881	2 T49279	hypothetical prote
25	42	53.8	1063	2 D71623	probable helicase
26	42	53.8	2441	2 A99291	erythrocyte membra
27	41.5	53.2	239	2 G90259	hypothetical prote
28	41.5	53.2	422	2 H90271	hypothetical prote
29	41.5	53.2	422	2 H90271	hypothetical prote

30	41.5	53.2	422	2 H90275	hypothetical prote
31	41	52.6	109	2 A86505	l31 ribosomal prot
32	41	52.6	109	2 H72118	ribosomal protein
33	41	52.6	115	2 S01281	hypothetical prote
34	41	52.6	200	2 B95057	hypothetical prote
35	41	52.6	200	2 B97926	rNA polymerase (de
36	41	52.6	224	2 T39771	hypothetical prote
37	41	52.6	277	2 D97067	probable xylanase/
38	41	52.6	285	2 T27458	hypothetical prote
39	41	52.6	399	2 T32933	cell-division prot
40	41	52.6	400	2 AB1565	6-phosphogluconate
41	41	52.6	472	2 AH1245	hypothetical prote
42	41	52.6	472	2 AD1509	hypothetical prote
43	41	52.6	552	2 T23526	hypothetical prote
44	41	52.6	552	2 S48328	hypothetical prote
45	41	52.6	648	2 T27412	polynucleotide pho
46	41	52.6	723	2 AC1241	polynucleotide pho
47	41	52.6	723	2 AG1603	ribonucleotide red
48	41	52.6	769	2 H97302	DNA topoisomerase
49	41	52.6	769	1 ISBT1	hypothetical prote
50	41	52.6	1359	2 T34036	hypothetical prote
51	40.5	51.9	422	2 H90501	pol polyproteins -
52	40	51.3	44	2 T09381	variance-associat
53	40	51.3	78	1 F64061	histone H2B-8 - wh
54	40	51.3	138	2 S56585	pol polyproteins -
55	40	51.3	148	2 A26192	hypothetical prote
56	40	51.3	155	2 H96761	hypothetical prote
57	40	51.3	203	2 F86145	p22L4.5 protein -
58	40	51.3	235	2 AD1735	hypothetical prote
59	40	51.3	251	2 T39332	hypothetical prote
60	40	51.3	278	2 S67432	hypothetical prote
61	40	51.3	289	2 B84098	pol polyproteins dia
62	40	51.3	427	2 T41257	hypothetical prote
63	40	51.3	504	2 D71615	hypothetical prote
64	40	51.3	521	2 T16692	hypothetical prote
65	40	51.3	522	2 C96608	hypothetical prote
66	40	51.3	820	2 C81252	probable NADH2 deh
67	40	51.3	839	2 T16753	hypothetical prote
68	40	51.3	902	2 T01668	pol polyproteins -
69	40	51.3	912	2 S33980	pol polyproteins -
70	40	51.3	1002	2 GNLJND	pol polyproteins -
71	40	51.3	1002	2 S54378	HIV-1 retropepsin
72	40	51.3	1003	1 GNMVUV	HIV-1 retropepsin
73	40	51.3	1003	1 B44001	HIV-1 retropepsin
74	40	51.3	1003	1 GNMVW2	pol polyproteins -
75	40	51.3	1003	2 T09440	HIV-1 retropepsin
76	40	51.3	1012	1 GNMVWL	HIV-1 retropepsin
77	40	51.3	1015	1 GNMVW3	DNA topoisomerase
78	40	51.3	1447	2 S02160	multitug resistanc
79	40	51.3	1545	1 S71841	calcium channel al
80	40	51.3	1851	2 T13980	posterior-group pr
81	40	51.3	2515	2 A41519	cell proliferation
82	40	51.3	2938	2 T30249	Gli protein - Amma
83	39	50.0	78	1 WZVZ53	hypothetical prote
84	39	50.0	101	2 G90536	histone H2B - whea
85	39	50.0	152	2 S22323	transcription regu
86	39	50.0	169	2 AD3110	hypothetical prote
87	39	50.0	179	2 S61904	transcription regu
88	39	50.0	201	2 H98176	hypothetical prote
89	39	50.0	205	2 T00865	hypothetical prote
90	39	50.0	226	2 S41032	ribosomal protein
91	39	50.0	277	2 AD1403	hypothetical prote
92	39	50.0	277	2 G96773	hypothetical prote
93	39	50.0	298	2 T39278	hypothetical prote
94	39	50.0	321	2 T19327	hypothetical prote
95	39	50.0	392	2 B36665	protein p22C12.16
96	39	50.0	411	2 S76760	transcription init
97	39	50.0	425	2 T21421	hypothetical prote
98	39	50.0	491	2 A46101	protein-tyrosine-p
99	39	50.0	535	2 S62508	probable U4/U6 sma
100	39	50.0	548	2 B46101	protein-tyrosine-p
101	39	50.0	548	2 T04465	hypothetical prote
102	39	50.0	557	2 T04465	hypothetical prote

hypothetical prote
l31 ribosomal prot
ribosomal protein
hypothetical prote
hypothetical prote
rNA polymerase (de
hypothetical prote
probable xylanase/
hypothetical prote
hypothetical prote
cell-division prot
6-phosphogluconate
hypothetical prote
hypothetical prote
polynucleotide pho
polynucleotide pho
ribonucleotide red
DNA topoisomerase
hypothetical prote
pol polyproteins -
variance-associat
histone H2B-8 - wh
pol polyproteins -
hypothetical prote
p22L4.5 protein -
hypothetical prote
hypothetical prote
pol polyproteins dia
hypothetical prote
hypothetical prote
hypothetical prote
probable NADH2 deh
hypothetical prote
pol polyproteins -
pol polyproteins -
HIV-1 retropepsin
HIV-1 retropepsin
HIV-1 retropepsin
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HIV-1 retropepsin
DNA topoisomerase
multitug resistanc
calcium channel al
posterior-group pr
cell proliferation
Gli protein - Amma
hypothetical prote
histone H2B - whea
transcription regu
hypothetical prote
transcription regu
hypothetical prote
hypothetical prote
ribosomal protein
hypothetical prote
hypothetical prote
hypothetical prote
protein p22C12.16
transcription init
hypothetical prote
protein-tyrosine-p
probable U4/U6 sma
protein-tyrosine-p
hypothetical prote

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OM protein - protein search, using SW model

Run on: May 5, 2006, 14:02:56 ; Search time 226 Seconds
(without alignments)
46.827 Million cell updates/sec

Title: US-10-666-851-2_COPY_217_231
Perfect score: 78
Sequence: 1 KKENGDKKIVPKKKK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Uniprot 05.80:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	158	1	SERP1_RAT
2	78	100.0	178	1	O6ZSL4_HUMAN
3	78	100.0	308	1	SERP1_BOVIN
4	78	100.0	314	1	SERP1_HUMAN
5	78	100.0	314	1	SERP1_MOUSE
6	78	100.0	314	2	O505A2_MOUSE
7	64	82.1	314	1	SERP1_CHICK
8	58	74.4	5229	2	O7RTP4_PLAYO
9	51	65.4	536	2	O64CC4_PARCH
10	50	64.1	311	2	O9Y124_XENLA
11	49	62.8	287	2	O614B0_CAEBR
12	49	62.8	308	2	O50YPS_ENTHI
13	49	62.8	326	2	O50OP4_ENTHI
14	49	62.8	758	2	O4RUV9_TETNG
15	48	61.5	310	2	O6TNR8_BRARE
16	48	61.5	321	2	O4SKX3_TETNG
17	47	60.3	297	2	O82W10_NITRU
18	47	60.3	348	2	O7RA45_PLAYO
19	47	60.3	425	2	O4YPAS_PLABR
20	47	60.3	610	2	O9LIH8_ARATH
21	46	59.0	136	2	O9WIS8_SHIV1
22	46	59.0	261	2	O4Y8S7_PLACH
23	46	59.0	278	1	O814L0_CAEBL
24	46	59.0	279	1	Y611_CAEBL
25	46	59.0	286	2	O909N2_SHIV1
26	46	59.0	315	2	O9AWG4_XENLA
27	46	59.0	315	2	O640J3_XENLA
28	46	59.0	315	2	O6GLS0_XENLA
29	46	59.0	324	2	O54Q96_DICDI
30	46	59.0	377	2	O4Z5H0_PLABR
31	46	59.0	397	1	YXX7_CAEBL

32	46	59.0	441	2	O5BEA8_BRARE	O5BEA8 brachydanio
33	46	59.0	510	2	O4V7X3_XENLA	O4V7X3 xenopus lae
34	46	59.0	532	2	O90W60_XENLA	O90W60 xenopus lae
35	46	59.0	713	2	O6PAX0_XENLA	O6PAX0 xenopus lae
36	46	59.0	715	2	O4Y8S2_PLACH	O4Y8S2 plasmodium
37	46	59.0	725	2	O965E8_ENTHI	O965E8 entamoeba h
38	46	59.0	819	2	O54UR9_DICDI	O54JF9 dictyostella
39	46	59.0	912	2	O6KER9_SHIV1	O6KER9 human immun
40	46	59.0	999	2	O4JG36_SHIV1	O4JG36 human immun
41	46	59.0	1002	2	O8USZ3_SHIV1	O8USZ3 human immun
42	46	59.0	1003	2	O8TBU7_SHIV1	O8TBU7 human immun
43	46	59.0	1010	2	O5K6U6_SHIVZ	O5K6U6 chimpanzee
44	46	59.0	1011	2	O8UTP1_SHIV1	O8UTP1 human immun
45	46	59.0	1012	2	O673V0_SHIV1	O673V0 human immun
46	46	59.0	1069	2	O519R3_ENTHI	O519R3 entamoeba h
47	46	59.0	1080	2	O510Y4_ENTHI	O510Y4 entamoeba h
48	46	59.0	1431	2	O8AE72_SHIV1	O8AE72 human immun
49	46	59.0	1433	2	O91R69_SHIV1	O91R69 human immun
50	46	59.0	1449	2	O910B0_SHIV1	O910B0 human immun
51	46	59.0	1449	2	O91DV9_SHIV1	O91DV9 human immun
52	46	59.0	18519	2	O8ISF6_CAEBL	O8ISF6 caenorhabdi
53	46	59.0	18534	2	O8ISF7_CAEBL	O8ISF7 caenorhabdi
54	46	57.7	65	2	O34700_BACSU	O34700 bacillus su
55	46	57.7	84	2	O4TF10_TETNG	O4TF10 tetratodon n
56	46	57.7	184	2	O7VVG5_BORPE	O7VVG5 bordetella
57	45	57.7	194	2	O7MAE5_BORPE	O7MAE5 bordetella
58	45	57.7	194	2	O7WJ18_BORPE	O7WJ18 bordetella
59	45	57.7	213	1	O4UR09_TREAN	O4UR09 trehalia a
60	45	57.7	315	1	SERP5_BOVIN	SERP5 bos taurus
61	45	57.7	317	1	SERP5_HUMAN	SERP5 homo sapien
62	45	57.7	350	2	O7RAP6_PLAYO	O7RAP6 plasmodium
63	45	57.7	418	2	O4S674_TETNG	O4S674 tetratodon n
64	45	57.7	493	2	O9SUD9_ARATH	O9SUD9 arabidopsis
65	45	57.7	574	2	O55C31_DICDI	O55C31 dictyostella
66	45	57.7	577	2	O7YZJ2_SMERT	O7YZJ2 halichondri
67	45	57.7	630	2	O4YN70_PLABR	O4YN70 plasmodium
68	45	57.7	699	2	O5FXS8_SHIV1	O5FXS8 human immun
69	45	57.7	714	2	O7RG16_PLABR	O7RG16 plasmodium
70	45	57.7	1055	2	O4XXY6_PLABR	O4XXY6 plasmodium
71	45	57.7	1089	2	O75B21_ASHCO	O75B21 ashbya gos8
72	44.5	57.1	289	2	O4YTF4_PLABR	O4YTF4 plasmodium
73	44.5	57.1	317	2	O4Y76_PLABR	O4Y76 plasmodium
74	44.5	57.1	516	2	O6AL11_DESP	O6AL11 desulfofale
75	44	56.4	273	2	O5AP68_CANAL	O5AP68 candida alb
76	44	56.4	278	2	O8D2B4_WIGBR	O8D2B4 wiggleswort
77	44	56.4	281	2	O568X0_BRARE	O568X0 brachydanio
78	44	56.4	296	2	O7T2K9_BRARE	O7T2K9 brachydanio
79	44	56.4	335	2	O9BLU5_ACYPI	O9BLU5 acyrtosiph
80	44	56.4	377	1	DNAJ_STRT1	DNAJ15 streptococc
81	44	56.4	377	1	DNAJ_STRT2	DNAJ15 streptococc
82	44	56.4	476	2	O4X1I6_PLACH	O4X1I6 plasmodium
83	44	56.4	502	2	O20240_CAEBL	O20240 caenorhabdi
84	44	56.4	562	2	O90038_VITRU	O90038 sebba virus
85	44	56.4	587	2	O59X38_CANAL	O59X38 candida alb
86	44	56.4	637	2	O5TXO0_ANOGA	O5TXO0 anopheles g
87	44	56.4	659	2	O6BK66_DEBHA	O6BK66 debaryowce
88	44	56.4	690	2	O7PCN5_ANOGA	O7PCN5 anopheles g
89	44	56.4	743	2	O6P1W7_HUMAN	O6P1W7 homo sapien
90	44	56.4	868	2	O503P4_BRARE	O503P4 brachydanio
91	44	56.4	919	2	O7Q942_ANOGA	O7Q942 anopheles g
92	44	56.4	972	2	O5TSL5_ANOGA	O5TSL5 anopheles g
93	44	56.4	1003	2	O69GR6_SHIV1	O69GR6 human immun
94	44	56.4	1003	2	O69GR7_SHIV1	O69GR7 human immun
95	44	56.4	1476	2	O5GBZ4_XENLA	O5GBZ4 xenopus lae
96	44	56.4	2378	2	O813U0_PLAF7	O813U0 plasmodium
97	44	56.4	4261	2	O81FP4_PLAF7	O81FP4 daucus caro
98	43.5	55.8	502	2	O803B3_DAUCA	O803B3 daucus caro
99	43	55.1	61	2	O81I08_PLAF7	O81I08 plasmodium
100	43	55.1	120	2	O95XH4_CAEBL	O95XH4 caenorhabdi
101	43	55.1	127	2	O4J7N1_GULAC	O4J7N1 sulfolobus
102	43	55.1	132	2	O9LZ45_ARATH	O9LZ45 arabidopsis
103	43	55.1	163	2	O8G117_ARATH	O8G117 arabidopsis
104	43	55.1	175	2	O9SVE4_ARATH	O9SVE4 arabidopsis

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OM protein - protein search, using SW model

Run on: May 5, 2006, 14:10:03 ; Search time 76 Seconds
(without alignments)
82.466 Million cell updates/sec

Title: US-10-666-851-2_COPY_217_231

Perfect score: 78
Sequence: 1 KKENGDKKIVPKKKK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10a_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10b_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	141	4	US-10-466-136-13 Sequence 13, Appl
2	78	100.0	229	4	US-10-425-586-8 Sequence 8, Appl1
3	78	100.0	229	4	US-10-466-136-8 Sequence 8, Appl1
4	78	100.0	267	4	US-10-425-586-7 Sequence 7, Appl1
5	78	100.0	267	4	US-10-466-136-7 Sequence 7, Appl1
6	78	100.0	313	3	US-09-796-008-2 Sequence 2, Appl1
7	78	100.0	313	4	US-10-138-434A-4 Sequence 4, Appl1
8	78	100.0	313	4	US-10-425-586-3 Sequence 3, Appl1
9	78	100.0	313	4	US-10-466-136-3 Sequence 3, Appl1
10	78	100.0	313	4	US-10-666-851-7 Sequence 7, Appl1
11	78	100.0	313	4	US-10-786-720-43 Sequence 43, Appl1
12	78	100.0	313	5	US-10-817-525-2 Sequence 2, Appl1
13	78	100.0	313	5	US-10-847-972-77 Sequence 77, Appl1
14	78	100.0	314	4	US-10-146-474-7 Sequence 7, Appl1
15	78	100.0	314	4	US-10-138-434A-3 Sequence 3, Appl1
16	78	100.0	314	4	US-10-301-764-7 Sequence 7, Appl1
17	78	100.0	314	4	US-10-666-851-2 Sequence 2, Appl1
18	78	100.0	314	4	US-10-788-792-148 Sequence 148, Appl
19	78	100.0	314	5	US-10-847-972-80 Sequence 80, Appl1
20	78	100.0	314	5	US-10-756-149-5611 Sequence 5611, Ap
21	78	100.0	338	4	US-10-425-586-4 Sequence 4, Appl1
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23	53	67.9	108	5	US-10-617-320-4788 Sequence 4788, Ap
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25	50	64.1	83	4	US-10-425-115-230293 Sequence 230293,
26	50	64.1	153	4	US-10-425-115-231235 Sequence 231235,
27	49	62.8	66	4	US-10-425-115-277499 Sequence 277499,

28	48	61.5	78	4	US-10-425-115-243409 Sequence 243409,
29	47	60.3	89	4	US-10-437-963-126220 Sequence 126220,
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47	45	57.7	317	4	US-10-146-474-6 Sequence 6, Appl1
48	45	57.7	317	4	US-10-338-604-2 Sequence 2, Appl1
49	45	57.7	317	4	US-10-301-764-6 Sequence 6, Appl1
50	45	57.7	317	5	US-10-768-566-1 Sequence 1, Appl1
51	45	57.7	816	4	US-10-425-115-280739 Sequence 280739,
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53	45	57.7	1018	4	US-10-369-294-46 Sequence 46, Appl1
54	45	56.4	43	4	US-10-424-599-148923 Sequence 148923,
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66	44	56.4	114	4	US-10-767-701-55041 Sequence 55041, A
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71	44	56.4	246	4	US-10-437-963-136903 Sequence 136903,
72	44	56.4	335	5	US-10-732-923-4505 Sequence 4505, Ap
73	44	56.4	587	4	US-10-032-585-7334 Sequence 7334, Ap
74	43	55.1	39	4	US-10-425-115-347711 Sequence 347711,
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79	43	55.1	51	4	US-10-437-963-125118 Sequence 125118,
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OM protein - protein search, using sw model

Run on: May 5, 2006, 14:02:26 ; Search time 184 Seconds
(without alignments)
35.819 Million cell updates/sec

Title: us-10-666-851-2_copy_217_231
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	78	100.0	229	5	ABR82249 Human sec
5	78	100.0	229	7	ADC71191 Deletion
6	78	100.0	229	8	ADH43313 Human sec
7	78	100.0	267	5	ABR82248 Human sec
8	78	100.0	267	7	ADC71190 Deletion
9	78	100.0	267	8	ADH43312 Human sec
10	78	100.0	313	4	AAE10154 Human sec
11	78	100.0	313	5	AAU07695 Human pri
12	78	100.0	313	5	ABR82244 Human sec
13	78	100.0	313	6	ABP72784 Human sec
14	78	100.0	313	7	ABR61428 Human emb
15	78	100.0	313	7	ADC71186 Human sec
16	78	100.0	313	8	ADH43308 Human sec
17	78	100.0	313	8	ADP68541 Human sec
18	78	100.0	313	8	ADU86503 Human sec
19	78	100.0	313	8	AE64566 Human lyp
20	78	100.0	313	9	ADV44810 Secreted
21	78	100.0	313	9	ADX58916 Human reg
22	78	100.0	314	2	AAW37817 Human sec
23	78	100.0	314	2	AAW88528 Human pri
24	78	100.0	314	6	ABP72785 Human sec

25	78	100.0	314	6	ABP72783	ABP72783 Human sFR
26	78	100.0	314	7	ABR61429	ABR61429 Murine em
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28	78	100.0	314	8	ADP68536	ADP68536 Human sec
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31	78	100.0	318	5	ABR82245	ABR82245 Human sec
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38	48	61.5	121	4	AAO05517	AAO05517 Human pol
39	47	60.3	31	2	AAH12916	AAH12916 Octopepti
40	46	59.0	128	4	AAO04686	AAO04686 Human pol
41	46	59.0	996	9	ADX39977	ADX39977 HIV pol p
42	46	59.0	1002	9	ADX39946	ADX39946 HIV pol p
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58	43	55.1	137	4	AAO03896	AAO03896 Human pol
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62	43	55.1	1002	9	ADX40058	ADX40058 HIV pol p
63	43	55.1	1278	3	ABH18277	ABH18277 Plasmodu
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68	42	53.8	195	3	AAH33061	AAH33061 Arabidops
69	42	53.8	226	7	ADR31137	ADR31137 Human dia
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73	42	53.8	292	4	ABH57977	ABH57977 Drosophi
74	42	53.8	295	3	AAH49439	AAH49439 Arabidops
75	42	53.8	297	3	AAH06973	AAH06973 Arabidops
76	42	53.8	314	6	ADH438292	ADH438292 Mouse sec
77	42	53.8	314	6	ADM67241	ADM67241 Murine ad
78	42	53.8	367	6	ADA83987	ADA83987 Human CDK
79	42	53.8	369	4	AAW79489	AAW79489 Human pro
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81	42	53.8	369	4	AAH41588	AAH41588 Human pol
82	42	53.8	424	4	ABH64433	ABH64433 Drosophi
83	42	53.8	455	7	ADC31549	ADC31549 Human nov
84	42	53.8	476	4	AAW78505	AAW78505 Human pro
85	42	53.8	500	4	AAH93943	AAH93943 Human pol
86	42	53.8	500	5	ABG95660	ABG95660 Human nuc
87	42	53.8	500	8	ADH44816	ADH44816 Human KXZ
88	42	53.8	500	8	ADL32095	ADL32095 Human pro
89	42	53.8	734	8	ADN22640	ADN22640 Bacteri
90	42	53.8	806	8	ADN22639	ADN22639 Bacteri
91	42	53.8	846	4	AAH39803	AAH39803 Human pol
92	42	53.8	861	7	ABH88619	ABH88619 Rice abio
93	42	53.8	881	5	ABH92593	ABH92593 Rice abio
94	42	53.8	897	5	ABH88650	ABH88650 Rice abio
95	42	53.8	920	7	AAH90383	AAH90383 Rice abio
96	42	53.8	955	4	AAH39802	AAH39802 Human pol
97	42	53.8	1146	8	ADP99073	ADP99073 C. albica

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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 14:06:06 ; Search time 1173 seconds
(without alignments)
9033.880 Million cell updates/sec

Title: US-10-666-851-1

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Gapop 10.0, Gapect 1.0

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Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	417.4	16.0	475	US-11-004-762-19	Sequence 19, App1
4	370.4	14.2	630	US-10-301-480-560598	Sequence 560598,
5	370.4	14.2	630	US-10-301-480-1174007	Sequence 1174007,
6	231.4	8.9	926	US-11-245-147-5	Sequence 5, App1
7	228	8.8	1382	US-11-245-147-197	Sequence 197, App
8	226.4	8.7	1196	US-10-216-161A-414	Sequence 414, App
9	176.6	6.8	1745	US-11-051-720-28	Sequence 28, App1
10	164.8	6.3	882	US-11-245-147-80	Sequence 80, App1
11	116.6	4.5	2379	US-09-925-065A-678403	Sequence 678403,
12	114	4.4	4350	US-11-245-147-124	Sequence 124, App
13	114	4.4	4350	US-11-245-147-125	Sequence 125, App
14	114	4.4	4350	US-11-245-147-205	Sequence 205, App

15	105	4.0	1944	US-11-245-147-49	Sequence 49, App1
16	103	4.0	631	US-09-925-065A-68204	Sequence 68204, A
17	103	4.0	631	US-10-301-480-169443	Sequence 169443,
18	103	4.0	631	US-10-301-480-782852	Sequence 782852,
19	101.2	3.9	1983	US-11-245-147-206	Sequence 206, App
20	97.4	3.7	4770	US-11-136-527-299	Sequence 299, App
21	97.2	3.7	1935	US-11-136-527-186	Sequence 186, App
22	87.8	3.4	2811	US-11-067-231-154	Sequence 154, App
23	87.8	3.4	2814	US-11-054-281-21	Sequence 21, App1
24	83.2	3.2	2184	US-11-054-281-35	Sequence 35, App1
25	77.2	3.0	2561	US-11-127-877-26	Sequence 26, App1
26	75.6	2.9	2820	US-11-186-284-188	Sequence 188, App
27	75.6	2.9	2820	US-11-245-147-204	Sequence 204, App
28	75.6	2.9	2840	US-11-054-281-23	Sequence 23, App1
29	73	2.8	1898	US-11-136-527-2690	Sequence 2690, Ap
30	73	2.8	7391	US-10-511-937-629	Sequence 629, App
31	73	2.8	7391	US-11-152-366-17	Sequence 17, App1
32	73	2.8	7392	US-11-169-041-5	Sequence 5, App1
33	73	2.8	7392	US-11-245-147-177	Sequence 177, App
34	73	2.8	7392	US-11-245-147-208	Sequence 208, App
35	61	2.3	2607	US-11-136-527-630	Sequence 630, App
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ALIGNMENTS

RESULT 1
US-11-245-147-203
; Sequence 203, Application US/11245147
; Publication No. US20060030541A1
GENERAL INFORMATION:
APPLICANT: GARCIA, TERESA
APPLICANT: ROMAN ROMAN, SERGIO
APPLICANT: BARON, ROLAND
APPLICANT: CALL, KATHERINE
APPLICANT: THREILHAR, JOACHIM
APPLICANT: CONNOLLY, TIMOTHY
APPLICANT: JACKSON, AMANDA
APPLICANT: BUSHNELL, STEVEN
APPLICANT: RANADI, GEORGES
TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
FILE REFERENCE: 37991-0023
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,400
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 203
LENGTH: 4469
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Homo sapiens secreted fibrinized-related protein 1
US-11-245-147-203

Query Match 94.8%; Score 2465.4; DB 18; Length 4469;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2553; Conservative 16; Indels 28; Gaps 5;

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 13:55:19 / Search time 1855 Seconds
(without alignments)
11599.419 Million cell updates/sec

Title: US-10-666-851-1
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2534.8	97.4	4500	6	US-10-138-434A-27 Sequence 27, Appl
3	2517.2	96.7	4462	3	US-09-974-298-28 Sequence 28, Appl
4	2465.4	96.8	4469	3	US-09-796-008-1 Sequence 1, Appl1
5	2465.4	96.8	4469	6	US-10-133-937-42 Sequence 42, Appl
6	2465.4	96.8	4469	6	US-10-172-118-857 Sequence 857, Appl
7	2465.4	96.8	4469	6	US-10-159-563-42 Sequence 42, Appl
8	2465.4	96.8	4469	7	US-10-342-887-857 Sequence 857, Appl
9	2465.4	96.8	4469	7	US-10-786-720-15 Sequence 15, Appl
10	2465.4	96.8	4469	8	US-10-788-792-21 Sequence 21, Appl
11	2465.4	96.8	4469	8	US-10-473-974-203 Sequence 203, Appl
12	2465.4	96.8	4469	8	US-10-817-525-1 Sequence 1, Appl1
13	2465.4	96.8	4469	9	US-10-756-149-3306 Sequence 3306, Appl
14	1803.8	69.3	2078	6	US-10-138-434A-1 Sequence 1, Appl1
15	1803.8	68.7	2075	6	US-10-138-434A-2 Sequence 2, Appl1
16	1787.8	68.7	2075	6	US-10-425-586-1 Sequence 1, Appl1
17	1787.8	68.7	2075	7	US-10-466-136-1 Sequence 1, Appl1
18	1483.4	57.0	3215	3	US-09-925-301-51 Sequence 51, Appl1
19	1076.2	41.4	1308	5	US-10-146-474-18 Sequence 18, Appl1
20	1076.2	41.4	1308	7	US-10-301-764-18 Sequence 18, Appl1
21	912.6	35.1	942	6	US-10-425-586-2 Sequence 2, Appl1
22	912.6	35.1	942	6	US-10-466-136-2 Sequence 2, Appl1
23	909.6	35.0	1017	6	US-10-425-586-9 Sequence 9, Appl1

24	697	26.8	804	6	US-10-425-586-12 Sequence 12, Appl1
25	634	24.4	741	6	US-10-425-586-11 Sequence 11, Appl1
26	603.2	23.2	2124	6	US-10-138-434A-26 Sequence 26, Appl
C 27	485.2	18.6	501	3	US-09-954-531-885 Sequence 885, Appl
C 28	485.2	18.6	501	3	US-09-954-531-1298 Sequence 1298, Appl
C 29	485.2	18.6	501	9	US-10-843-641A-1952 Sequence 1952, Appl
C 30	485.2	18.6	501	9	US-10-843-641A-2365 Sequence 2365, Appl
C 31	481.6	18.5	588	6	US-10-425-586-10 Sequence 10, Appl1
C 32	444	17.1	690	6	US-10-425-586-13 Sequence 13, Appl1
C 33	427.6	16.4	445	7	US-10-242-535A-43352 Sequence 43352, Appl
C 34	427.6	16.4	445	7	US-10-388-604-1 Sequence 1, Appl1
C 35	401.2	15.4	1905	6	US-10-338-604-1 Sequence 2, Appl1
C 36	401.2	15.4	1905	8	US-10-768-566-2 Sequence 5, Appl1
C 37	401.2	15.4	1984	7	US-10-146-474-5 Sequence 5, Appl1
C 38	401.2	15.4	1984	7	US-10-301-764-5 Sequence 3, Appl1
C 39	395	15.2	954	6	US-10-338-604-3 Sequence 4, Appl1
C 40	394.2	15.1	1186	6	US-10-338-604-4 Sequence 6, Appl1
C 41	388.4	14.9	945	6	US-10-338-604-6 Sequence 95, Appl1
C 42	255.8	9.8	271	3	US-09-968-007A-95 Sequence 103, Appl
C 43	255.8	9.8	271	3	US-09-968-007A-303 Sequence 6565, Appl
C 44	255.8	9.8	271	3	US-10-843-641A-6565 Sequence 6773, Appl
C 45	255.8	9.8	271	9	US-10-843-641A-6773 Sequence 6773, Appl

ALIGNMENTS

RESULT 1									
US-10-666-851-1									
Sequence 1, Application US/10666851									
Publication No. US20040115195A1									
GENERAL INFORMATION:									
APPLICANT: Bodine, Peter									
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING SECRETED FRIZZLED									
FILE REFERENCE: 00630/1000091-US1									
CURRENT APPLICATION NUMBER: US/10/666,851									
CURRENT FILING DATE: 2003-09-19									
PRIOR APPLICATION NUMBER: US 10/169,545									
PRIOR FILING DATE: 2002-05-31									
PRIOR APPLICATION NUMBER: US 60/412,379									
PRIOR FILING DATE: 2002-09-19									
NUMBER OF SEQ ID NOS: 30									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 1									
LENGTH: 2602									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-10-666-851-1									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	121	GCGCATCGGCGCGACGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT	180						
QY	181	GCGCGCGGCGCTTGGCGCGGCGCTTGGCGCGAGGAGTACGTAAGCTTCCAGTC	240						
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 09:55:34 / Search time 2747 Seconds
(without alignments)
6312.898 Million cell updates/sec

Title: US-10-666-851-1

Perfect score: 2602
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Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 496897 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2533.2	97.4	4497	2 AAV84395	AAV84395 Human Frl
5	2517.2	96.7	4462	8 ABX77526	ABX77526 Different
6	2465.4	94.8	4469	4 AAS12954	AAS12954 Human Frl
7	2465.4	94.8	4469	6 ABT10165	ABT10165 Human bre
8	2465.4	94.8	4469	6 ABZ34845	ABZ34845 Coding se
9	2465.4	94.8	4469	12 ADP21417	ADP21417 Gene SFRP
10	2465.4	94.8	4469	13 ADR24996	ADR24996 Breast ca
11	2465.4	94.8	4469	13 ADR99015	ADR99015 Secreted
12	2465.4	94.8	4469	13 AEA64538	AEA64538 Human lyp
13	2465.4	94.8	4469	14 ADV44809	ADV44809 Secreted
14	2465.4	94.8	4469	14 ADX58915	ADX58915 Human reg
15	2382.8	88.5	4245	4 AAF80506	AAF80506 Cell prol
16	1927.4	74.1	3670	2 AAZ33577	AAZ33577 Human bre
17	1871.4	71.9	3872	13 ADR07183	ADR07183 Full leng
18	1844.6	70.9	2094	8 ABZ82228	ABZ82228 Human sec
19	1787.8	68.7	2075	4 AAD17401	AA17401 Human sec

20	1787.8	68.7	2075	6 ABV73022	ABV73022 Human sec
21	1787.8	68.7	2075	8 ABX75330	ABX75330 Human CDN
22	1787.8	68.7	2075	8 AAD52558	AA52558 FRP DNA.
23	1787.8	68.7	2075	12 ADH43319	ADH43319 Human sec
24	1787.4	68.7	2075	10 ADCT1197	ADCT1197 Human sec
25	1781.6	68.5	2072	8 ABZ81830	ABZ81830 Receptor
26	1483.4	57.0	3215	3 AAC77657	AAC77657 Human can
27	1458.4	56.4	3216	2 AAZ33608	AAZ33608 Human bre
28	1452.8	55.8	3180	2 AAZ42127	AAZ42127 Human nor
29	1076.2	41.4	1308	2 AAV19115	AAV19115 Human sec
30	996.4	38.3	1247	13 ACN41451	ACN41451 Human dia
31	925.8	35.6	942	8 ABZ82227	ABZ82227 Human sec
32	925.8	35.6	942	9 ACC81035	ACC81035 Human emb
33	912.6	35.1	942	6 ABV73023	ABV73023 Human sec
34	912.6	35.1	942	10 ADCT1198	ADCT1198 ORF of th
35	912.6	35.1	942	12 ADH43320	ADH43320 Human sec
36	909.6	35.0	1017	10 ADH43314	ADH43314 Human sFR
37	909.6	35.0	1017	12 ADH43314	ADH43314 Murine em
38	829.8	31.9	945	9 ACC81034	ACC81034 DNA encod
39	697	26.8	804	10 ADCT1195	ADCT1195 Human sec
40	697	26.8	804	12 ADH43317	ADH43317 Human sec
41	697	26.8	741	10 ADCT1194	ADCT1194 DNA encod
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45	628.8	24.2	1146	8 ABZ81842	ABZ81842 WIF-1 nuc

ALIGNMENTS

RESULT 1
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ID ADP68535 standard; DNA; 2602 BP.

ADP68535;

09-SEP-2004 (first entry)

Human secreted frizzled related protein, sFRP-1, DNA.

de; gene: bone-formation; secreted frizzled related protein; sFRP;
bone disorder; bone formation disorder; bone resorption disorder;
bone density disorder; degenerative bone disorder;
osteodysplasia; osteoporosis; osteopenia; osteoarthritis; osteoporosis;
type II osteoporosis; human; sFRP-1.

Homo sapiens.

Key Location/Qualifiers
CDS 119..1063
/*tag= a
/product= "sFRP-1"

US2004115195-A1.

17-JUN-2004.

19-SEP-2003; 2003US-0066851.

31-MAY-2002; 2002US-00169545.
PR 19-SEP-2002; 2002US-0412379P.

(BOD1/) BODINE P.

Bodine P;

WPI; 2004-449339/42.

P-PSDB; ADP68536.

New compositions comprising secreted frizzled related protein (sFRP),
anti-sFRP antibody, nucleic acid encoding sFRP or the antibody, or sFRP
antisense nucleic acids, for regulating bone-forming activity or treating

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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 13:22:06 ; Search time 12942 Seconds

(without alignment)
11428.424 Million cell updates/sec

Title: US-10-666-851-1

Perfect score: 2602
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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	2465.4	94.8	4469	6	CS025753 Sequence
5	2465.4	94.8	4469	6	AX236302 Sequence
6	2465.4	94.8	4469	6	AX578081 Sequence
7	2465.4	94.8	4469	8	AF056087 Homo sapi
8	2302.8	88.5	4245	6	BR135188 Sequence
9	1927.4	74.1	3670	6	BD135188 Human nuc
10	1927.4	74.1	3670	6	AX017498 Sequence
11	1871.4	71.9	3872	6	CO850220 Sequence
12	1871.4	71.9	3872	8	AK127331 Homo sapi
13	1844.6	70.9	2094	8	AF017987 Homo sapi
14	1803.8	69.3	2078	8	AR253205 Sequence
15	1802.8	69.3	17133	8	AC103846 Homo sapi
16	1802.8	69.3	188270	8	AC104393 Homo sapi
17	1787.8	68.7	2075	6	AR253206 Sequence
18	1787.8	68.7	2075	6	AR361924 Sequence

19	1787.8	68.7	2075	6	AR433000 Sequence
20	1787.8	68.7	2075	6	AX482567 Sequence
21	1787.8	68.7	2075	6	AX565707 Sequence
22	1787.8	68.7	2075	6	AX597107 Sequence
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35	885	34.0	2659	9	MM088566 Mus muscu
36	874.2	33.6	1340	5	BC024495 Mus muscu
37	721.2	27.7	3065	5	GGA404652 Gallus ga
38	697	26.8	804	6	AR361929 Sequence
39	656.8	25.2	15591	8	AC016868 Homo sapi
40	634	24.4	741	6	AR361928 Sequence
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42	628.8	24.2	1146	6	AX597129 Sequence
43	628.8	24.2	1146	6	AX701375 Sequence
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ALIGNMENTS

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ACCESSION	AX099741.1	GI:13538784			
VERSION					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Bodine, P.V.				
TITLE	Pharmaceutical compositions and methods of using secreted fibrinized related protein				
JOURNAL	Patent: WO 0119855-A 1 22-MAR-2001;				
FEATURES	American Home Products Corporation (US)				
source	1..2602				
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QY	61 GGGCGGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 120				
DB	61 GGGCGGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 120				
QY	121 GGGCATTCGGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGT 180				
DB	121 GGGCATTCGGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGT 180				